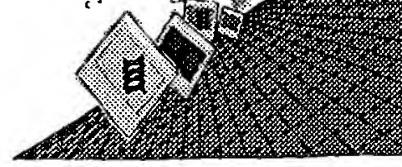


Sorbe

RAW SEQUENCE LISTING ERROR REPORT

BIOTECH LOGY
SYSTEMS
BRANCH



#81308
5/3/01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/515,369

RECEIVED

Source: 1633

MAY - 1 2001

Date Processed by STIC: 4/22/2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/515,369

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 Use of <220>Feature (NEW RULES) Sequence(s) 2-13 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

E. Sorbello

1633

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Fisher, Paul
 4 Madireddi, Malavi
 6 <120> TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED GENE-7 PROMOTER AND USES THEREOF
 8 <130> FILE REFERENCE: 0575/56778/JPW/APE
 10 <140> CURRENT APPLICATION NUMBER: 09/515,369
 11 <141> CURRENT FILING DATE: 2000-02-29
 13 <160> NUMBER OF SEQ ID NOS: 13
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2286
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Human
 22 <400> SEQUENCE: 1

23	taatacact cactataggg cgtcgactcg atcacctttt gaacccaggt ctgcctgcct	60
25	ccaaagctt tactcataac tagatttca actgatgttggccaaagggtt cctagtttct	120
27	ctccttgacc ttcccttctga agtaataatg ctatgataag ctcatcgagg gctgaggccc	180
29	aggcacatgt ttgcctgaac tatccatgtt atatgattcc ttccctcagac agagtggact	240
31	actcacgatc ccagggtgtac cctgaggcca gccaaagggtt atccatgacc tcattgcctct	300
33	gttcaggcct gcccctttaac agctcatccc acctgcttgc cctccccccc tatctgcaga	360
35	cagtagtcta ggatttcagc tgccctgggg gtcatttttcc ctcttcagct tcctgttta	420
37	gctgtcttccct gcctcccaact cacctattac tccagcactc tcacctggc ttcttttctg	480
39	tctcatcaact gcctcttgcac atctttatct catagtagtt agttaggggt tcttggtaat	540
41	gcccctaaatc cacatggtgga aagggggggaa gtggggggaaag agagtgcgt gtggggctgt	600
43	gcctacttct ggagggttaag actcggggcc tccaggaaca aaggattcag gctgggtggca	660
45	gctatagcca agcagactgc tggccaggga ttgcaaaaggaa gtatttttgtt tgcttaagaa	720
47	aataaacaac actgagatgtt agatggaggga agggggtgtt ggtgccagag agattggaa	780
49	gagtcgtccca agggtgtgtt ctactcaactc tccttttttc ttctcatctcc actgagactgg	840
51	aggcagttat cctgtcccccc acgtcacatt ctactcccg ttccatgc ctggaccagg	900
53	gttgggcaaa ctcttcctgt aaagaaccag acaggaacta tttaggcctc tggccat	960
55	atggctcag tcacaactac tcatctctgc ctgtgtagca cgaaagcaat tagcaacaat	1020
57	atgtcaacaa acatatgtga ccccatgaaa acttttatttta ttatggatc ggaaacactga	1080
59	aaataatgtc ttcttttttttgc ttttttcccc aatcattaaa aaacgtaaaaa actacttta	1140
61	ggtcgaagg ttaagccatt ctcagcttag cagttggcagg ctggattttgg cttgtgacct	1200
63	acagttggcc aatccctgtat tcccaaaatgttatttcctcag ggtatgtggc aaataacttat	1260
65	gggaagtgtt ggtttaaaca ggtttaagaa gcatcagaca ttccaggac gggctagcac	1320
67	atgcaggcgc tctctaaactg accttcattgg atttcattgtt ttcatggggg atcttgcag	1380
69	acaagaattc ctcaaaccata gagtctgggg actgtgtttt gggaaacact gctctgttgc	1440
71	atgccttcac tgggcacatgt gttagaatcta gagtcgttgc ctttgcgttgc tggagatagg	1500
73	gtcagagctc ttgactgccc tggcagtttgc gacacatcac gttgtctgtg tccctgtgt	1560
75	ggttcagagc cacacaggcc aagacttagcc caccagagca ccaggcctcc cagtttctg	1620
77	ggctgttcca tgcgtacatt tccttatttcc ttctgggttcc cagaacctaa ggagaggcac	1680
79	atttgggttgc agtggattata acccttaggg ccatgggttag ctgcgttgc gggaaacactc	1740
81	ctcaacttcc tggccctgtat ggattaaagg agaggttactt acaggttattt tcttcgtgt	1800
83	ggactactgtt cccagcatga atagggcatc attattgtat tattttgaca ggaaggagac	1860
85	tgggttatgc tgcacagttaa taatgtatcc acatgtgtac agagtttacc aagcacctct	1920
87	gtgtgtttttt tgcctttgtt tattacactt gggacaattt tttaaaattt atacatgcag	1980
89	agactgcaggc gcaagaaaggc taagaaactt qcccccgtcccc acacagccag tggtagagcc	2040

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

91 tgaactcaa cccaggcttc atctcaccc aggggctgct ttccccatcg ctgtattgtc 2100
93 cttaaagtga tgggtgacta ggcaatgaag taattctcta ggaaagcatg accaatttcc 2160
95 ctttctccac ctccctcttt ttccctccacc cctccccat cagccccat atatatgccc 2220
97 aaatctccac aaagccttgc ttgcctgcaa acctttactt ctgaaatgac ttccacggct 2280
99 gggacg 2286
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 21
104 <212> TYPE: DNA
C--> 105 <213> ORGANISM: Artificial
W--> 107 <220> FEATURE:
W--> 107 <223> OTHER INFORMATION:
107 <400> SEQUENCE: 2
108 cgtcccaagcc gtggaaagtca t 21
111 <210> SEQ ID NO: 3
112 <211> LENGTH: 21
113 <212> TYPE: DNA
C--> 114 <213> ORGANISM: Artificial
W--> 116 <220> FEATURE:
W--> 116 <223> OTHER INFORMATION:
116 <400> SEQUENCE: 3
117 aggctggatt tggcttgtga c 21
120 <210> SEQ ID NO: 4
121 <211> LENGTH: 21
122 <212> TYPE: DNA
C--> 123 <213> ORGANISM: Artificial
W--> 125 <220> FEATURE:
W--> 125 <223> OTHER INFORMATION:
125 <400> SEQUENCE: 4
126 ctgtttaatc cagcacttcc c 21
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 21
131 <212> TYPE: DNA
C--> 132 <213> ORGANISM: Artificial
W--> 134 <220> FEATURE:
W--> 134 <223> OTHER INFORMATION:
134 <400> SEQUENCE: 5
135 cgcttgatga ctcagccgga a 21
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 20
140 <212> TYPE: DNA
C--> 141 <213> ORGANISM: Artificial
W--> 143 <220> FEATURE:
W--> 143 <223> OTHER INFORMATION:
143 <400> SEQUENCE: 6
144 tgcagatgc gcaatctgca 20
147 <210> SEQ ID NO: 7
148 <211> LENGTH: 21
149 <212> TYPE: DNA
C--> 150 <213> ORGANISM: Artificial

(global
errors)

see item 11 on Ema Summary Sheet
→ see item 12 on Ema Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:03

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

W--> 152 <220> FEATURE:
W--> 152 <223> OTHER INFORMATION:
152 <400> SEQUENCE: 7
153 cgcttgatga cttggccgga a 21
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 22
158 <212> TYPE: DNA
C--> 159 <213> ORGANISM: Artificial
W--> 161 <220> FEATURE:
W--> 161 <223> OTHER INFORMATION:
161 <400> SEQUENCE: 8
162 tgcagagaga ctatgtctcg ca 22
165 <210> SEQ ID NO: 9
166 <211> LENGTH: 61
167 <212> TYPE: DNA
C--> 168 <213> ORGANISM: Artificial
W--> 170 <220> FEATURE:
W--> 170 <223> OTHER INFORMATION:
170 <400> SEQUENCE: 9
171 uuguaauua uacaacucua uuuuaauua gucaguauu caacugaagu ucuauuuauu 60
173 u 61
176 <210> SEQ ID NO: 10
177 <211> LENGTH: 15
178 <212> TYPE: DNA
C--> 179 <213> ORGANISM: Artificial
W--> 181 <220> FEATURE:
W--> 181 <223> OTHER INFORMATION:
181 <400> SEQUENCE: 10
182 uauuuauuaa uuuua 15
185 <210> SEQ ID NO: 11
186 <211> LENGTH: 51
187 <212> TYPE: DNA
C--> 188 <213> ORGANISM: Artificial
W--> 190 <220> FEATURE:
W--> 190 <223> OTHER INFORMATION:
190 <400> SEQUENCE: 11
191 uaaauuuaua auauuuauau uuuuaaaaaua uuuauuuauu uauuuauuuua a 51
194 <210> SEQ ID NO: 12
195 <211> LENGTH: 34
196 <212> TYPE: DNA
C--> 197 <213> ORGANISM: Artificial
W--> 199 <220> FEATURE:
W--> 199 <223> OTHER INFORMATION:
199 <400> SEQUENCE: 12
200 auuauuuauu auuuauuuau uauuuauuuua uuuu 34
203 <210> SEQ ID NO: 13
204 <211> LENGTH: 56
205 <212> TYPE: DNA
C--> 206 <213> ORGANISM: Artificial

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001

TIME: 14:17:03

Input Set : A:\56778.txt

Output Set: N:\CRF3\04222001\I515369.raw

W--> 208 <220> FEATURE:

W--> 208 <223> OTHER INFORMATION:

208 <400> SEQUENCE: 13

209 guuuuuuaauu uaauuaauua gauggauucu cagauauuuua uaauuuuuauu uuauuu

56

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/515,369

DATE: 04/22/2001
TIME: 14:17:04

Input Set : A:\56778.txt
Output Set: N:\CRF3\04222001\I515369.raw

L:105 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:107 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:107 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:114 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:116 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:123 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:125 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:125 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:132 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:134 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:134 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:141 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:143 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:143 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:150 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:152 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:152 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:159 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:161 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:161 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:168 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:170 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:170 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:179 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:181 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:181 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:188 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:190 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:190 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:197 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:199 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:199 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:206 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:208 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:208 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: